

FIG.1

5' -GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAATAATTCGATTGCTGTACC-
+-----+-----+-----+-----+-----+-----+-----+-----+
D S V C P Q G K Y I H P Q N N S I C C T -
-AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGCAGGATACGGAC-
+-----+-----+-----+-----+-----+-----+-----+-----+
K C H K G T Y L Y N D C P G P G Q D T D -
-TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC-
+-----+-----+-----+-----+-----+-----+-----+-----+
C R E C E S G S F T A S E N H L R H C L -
-AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC-
+-----+-----+-----+-----+-----+-----+-----+-----+
S C S K C R K E M G Q V E I S S C T V D -
-CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTT-
+-----+-----+-----+-----+-----+-----+-----+-----+
R D T V C G C R K N Q Y R H Y W S E N L -
-TTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG-
+-----+-----+-----+-----+-----+-----+-----+-----+
F Q C F N C S L C L N G T V H L S C Q E -
-AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC-
+-----+-----+-----+-----+-----+-----+-----+-----+
K Q N T V C T C H A G F F L R E N E C V -
-TCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGTGCCTACCCCAGATTGAG-
+-----+-----+-----+-----+-----+-----+-----+-----+
S C S N C K K S L E C T K L C L P Q I E -
-AAT-3'
+-----+
N *

FIG.2

5' -CATATGGACAGCGTTTGCCCCCAAGGAAAATACATCCACCCTCAAATAATTTCGATTTGC-
+-----+-----+-----+-----+-----+-----+-----+-----+
M D S V C P Q G K Y I H P Q N N S I C -
-TGTACCAAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGAT-
+-----+-----+-----+-----+-----+-----+-----+-----+
C T K C H K G T Y L Y N D C P G P G Q D -
-ACGGACTGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACAC-
+-----+-----+-----+-----+-----+-----+-----+-----+
T D C R E C E S G S F T A S E N H L R H -
-TGCCTCAGCTGCTCCAAATGCCGAAAGGAAATGGGTGAGGTGGAGATCTCTTCTTGCACA-
+-----+-----+-----+-----+-----+-----+-----+-----+
C L S C S K C R K E M G Q V E I S S C T -
-GTGGACCGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAA-
+-----+-----+-----+-----+-----+-----+-----+-----+
V D R D T V C G C R K N Q Y R H Y W S E -
-AACCTTTTCCAGTGCTTCTGCTGATAGGATCC-3'
+-----+-----+-----+-----+-----+-----+-----+-----+
N L F Q C F C *

FIG.3

5' -CATATGGACA GCGTTTGCCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTTCG-
+-----+-----+-----+-----+-----+-----+-----+-----+
M D S V C P Q G K Y I H P Q N N S I C -
-TGTACCAAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCCGGGGCAGGAT-
+-----+-----+-----+-----+-----+-----+-----+-----+
C T K C H K G T Y L Y N D C P G P G Q D -
-ACGGACTGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCCACCTCAGACAC-
+-----+-----+-----+-----+-----+-----+-----+-----+
T D C R E C E S G S F T A S E N H L R H -
-TGCCTCAGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACA-
+-----+-----+-----+-----+-----+-----+-----+-----+
C L S C S K C R K E M G Q V E I S S C T -
-GTGGACCGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAA-
+-----+-----+-----+-----+-----+-----+-----+-----+
V D R D T V C G C R K N Q Y R H Y W S E -
-AACCTTTTCCAGTGCTTCAATTGCTCTCTGTAAAAGCTT-3'
+-----+-----+-----+-----+-----+-----+-----+-----+
N L F Q C F N C S L *

FIG.4

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5' - CATATGGACAGCGTTTGCCCCAAGGAAATATATCCACCCTCAAATAATTGATTTC -
+-----+-----+-----+-----+-----+-----+-----+-----+
  M  D  S  V  C  P  Q  G  K  Y  I  H  P  Q  N  N  S  I  C  -
- TGTACCAAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGCAGGAT -
+-----+-----+-----+-----+-----+-----+-----+-----+
  C  T  K  C  H  K  G  T  Y  L  Y  N  D  C  P  G  P  G  Q  D  -
- ACGGACTGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACAC -
+-----+-----+-----+-----+-----+-----+-----+-----+
  T  D  C  R  E  C  E  S  G  S  F  T  A  S  E  N  H  L  R  H  -
- TGCCTCAGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACA -
+-----+-----+-----+-----+-----+-----+-----+-----+
  C  L  S  C  S  K  C  R  K  E  M  G  Q  V  E  I  S  S  C  T  -
- GTGGACCGGGACACCGTGTGTGGTTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAA -
+-----+-----+-----+-----+-----+-----+-----+-----+
  V  D  R  D  T  V  C  G  C  R  K  N  Q  Y  R  H  Y  W  S  E  -
- AACCTTTTCCAGTGCTTCAATTAATAGGGATCC - 3'
+-----+-----+-----+-----+-----+-----+-----+-----+
  N  L  F  Q  C  F  N  *

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FIG.5

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5' -CATATGTATATCCACCCTCAAAATAATTGATTTGCTGTACCAAGTGCCACAAAGGAACC-
+-----+-----+-----+-----+-----+-----+-----+-----+
  M  Y  I  H  P  Q  N  N  S  I  C  C  T  K  C  H  K  G  T  -
- TACTTGTACAATGACTGTCCAGGCCCGGGCAGGATACGGACTGCAGGGAGTGTGAGAGC-
+-----+-----+-----+-----+-----+-----+-----+-----+
  Y  L  Y  N  D  C  P  G  P  G  Q  D  T  D  C  R  E  C  E  S  -
- GGCTCCTTCACCGCTTCAGAAAACCACTCAGACACTGCCTCAGCTGCTCCAAATGCCGA-
+-----+-----+-----+-----+-----+-----+-----+-----+
  G  S  F  T  A  S  E  N  H  L  R  H  C  L  S  C  S  K  C  R  -
- AAGGAAATGGGTCAGGTGGAGATCTCTTCTTGACAGTGGACCGGGACACCGTGTGTGGC-
+-----+-----+-----+-----+-----+-----+-----+-----+
  K  E  M  G  Q  V  E  I  S  S  C  T  V  D  R  D  T  V  C  G  -
- TGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTTTTCCAGTGCTTCAATTGC-
+-----+-----+-----+-----+-----+-----+-----+-----+
  C  R  K  N  Q  Y  R  H  Y  W  S  E  N  L  F  Q  C  F  N  C  -
- TCTCTGTAAAAGCTT-3'
+-----+-----+-----+-----+-----+-----+-----+-----+
  S  L  *

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FIG.6

5' -CATATGTGTACCAAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGG-
+-----+-----+-----+-----+-----+-----+-----+-----+
M C T K C H K G T Y L Y N D C P G P G -
-CAGGATACGGACTGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCCACCTC
+-----+-----+-----+-----+-----+-----+-----+-----+
Q D T D C R E C E S G S F T A S E N H L -
-AGACACTGCCTCAGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCT-
+-----+-----+-----+-----+-----+-----+-----+-----+
R H C L S C S K C R K E M G Q V E I S S -
-TGCACAGTGGACCGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGG-
+-----+-----+-----+-----+-----+-----+-----+-----+
C T V D R D T V C G C R K N Q Y R H Y W -
-AGTGAAAACCTTTTCCAGTGCTTCAATTGCTCTCTGTAAAAGCTT-3'
+-----+-----+-----+-----+-----+-----+-----+-----+
S E N L F Q C F N C S L *

FIG.7

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5' -CATATGTCGATTAGCTGTACCAAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCA-
+-----+-----+-----+-----+-----+-----+-----+-----+
  M  S  I  S  C  T  K  C  H  K  G  T  Y  L  Y  N  D  C  P  -
-
-GGCCCCGGGGCAGGATACGGACTGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAA-
+-----+-----+-----+-----+-----+-----+-----+-----+
  G  P  G  Q  D  T  D  C  R  E  C  E  S  G  S  F  T  A  S  E  -
-
-AACCACCTCAGACACTGCCTCAGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAG-
+-----+-----+-----+-----+-----+-----+-----+-----+
  N  H  L  R  H  C  L  S  C  S  K  C  R  K  E  M  G  Q  V  E  -
-
-ATCTCTTCTTGACAGTGGACCGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGG-
+-----+-----+-----+-----+-----+-----+-----+-----+
  I  S  S  C  T  V  D  R  D  T  V  C  G  C  R  K  N  Q  Y  R  -
-
-CATTATTGGAGTGAAAACCTTTTCCAGTGCTTCAATTGCTCTCTGTAAAAGCTT-3'
+-----+-----+-----+-----+-----+-----+-----+-----+
  H  Y  W  S  E  N  L  F  Q  C  F  N  C  S  L  *

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FIG. 10

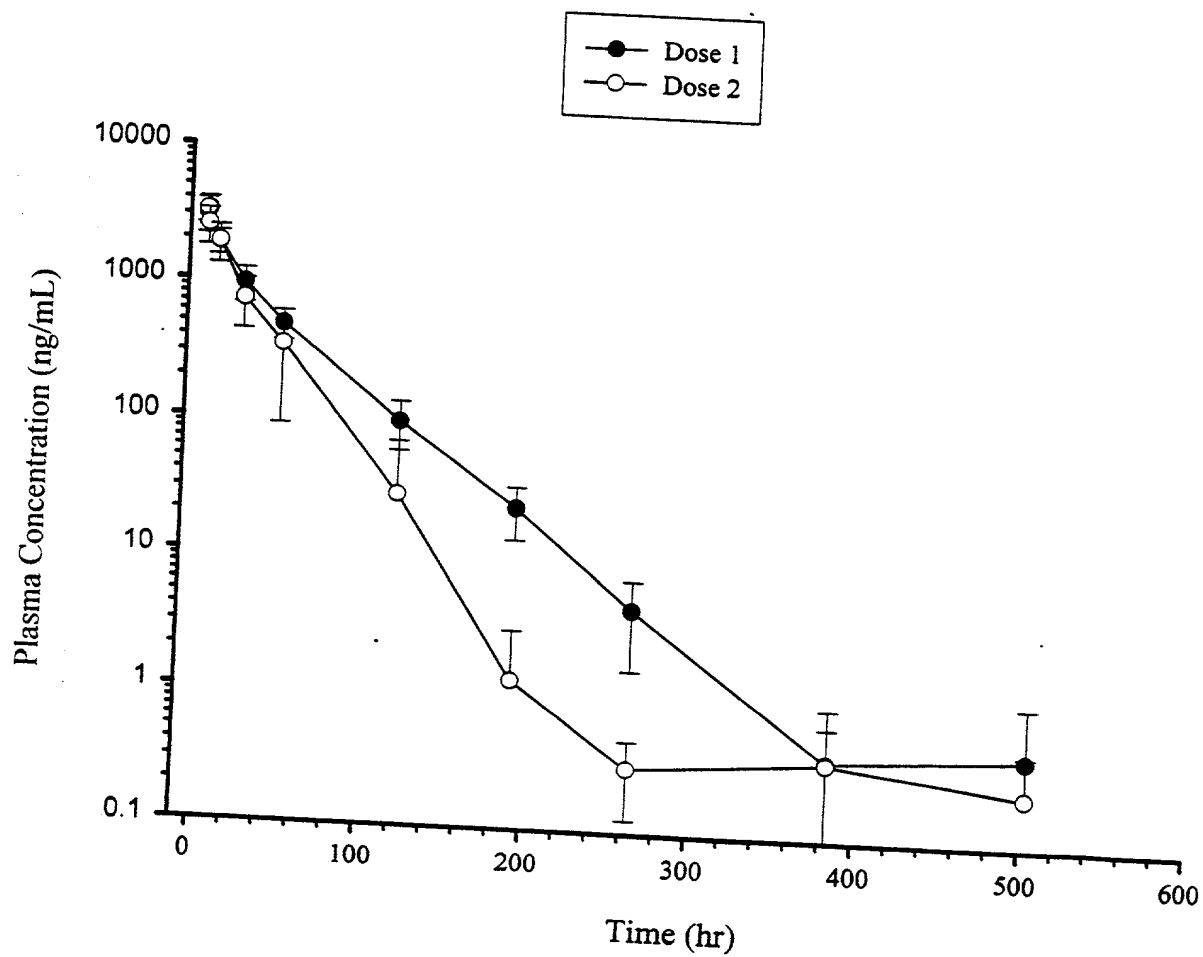


FIG. 11

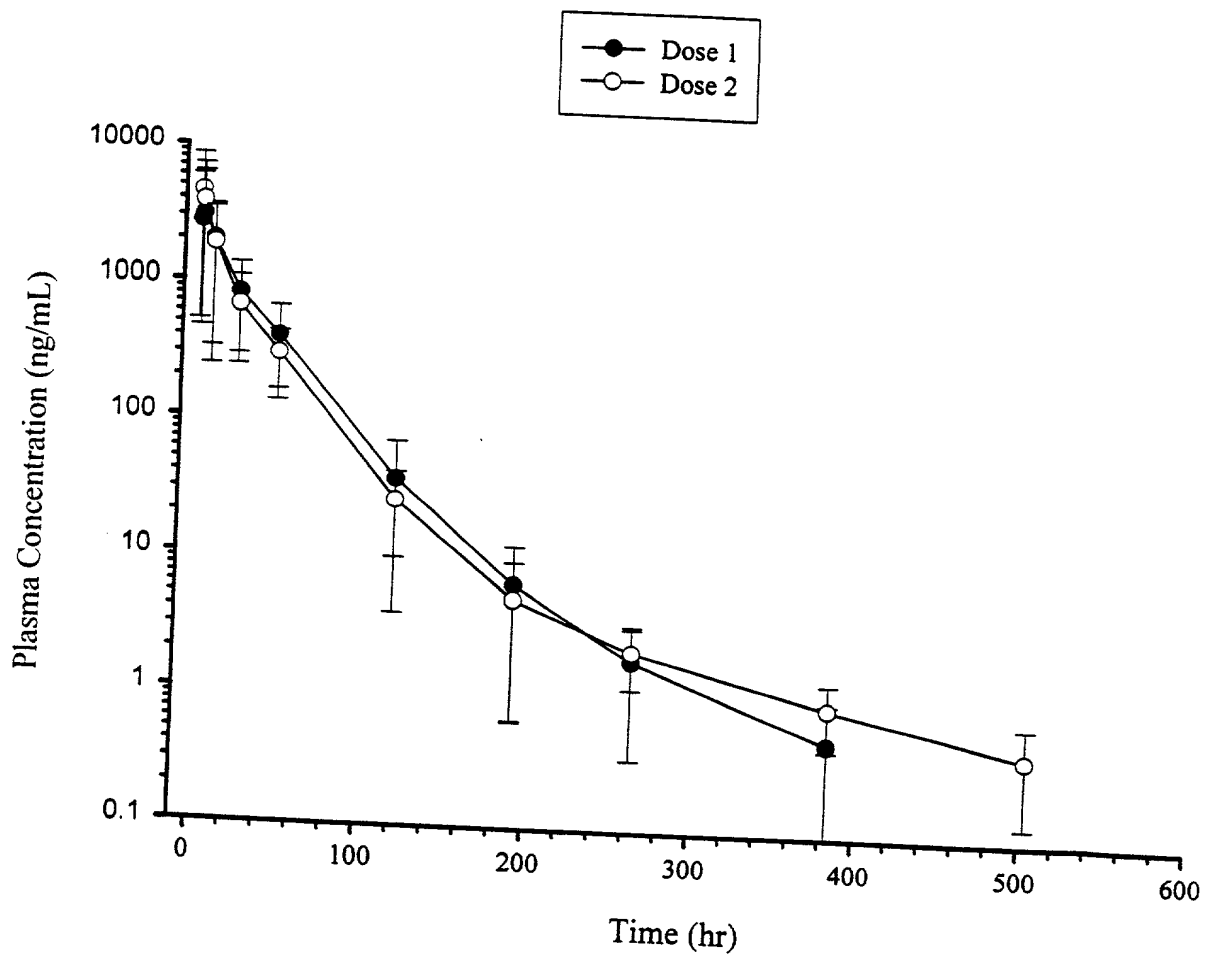


FIG. 12

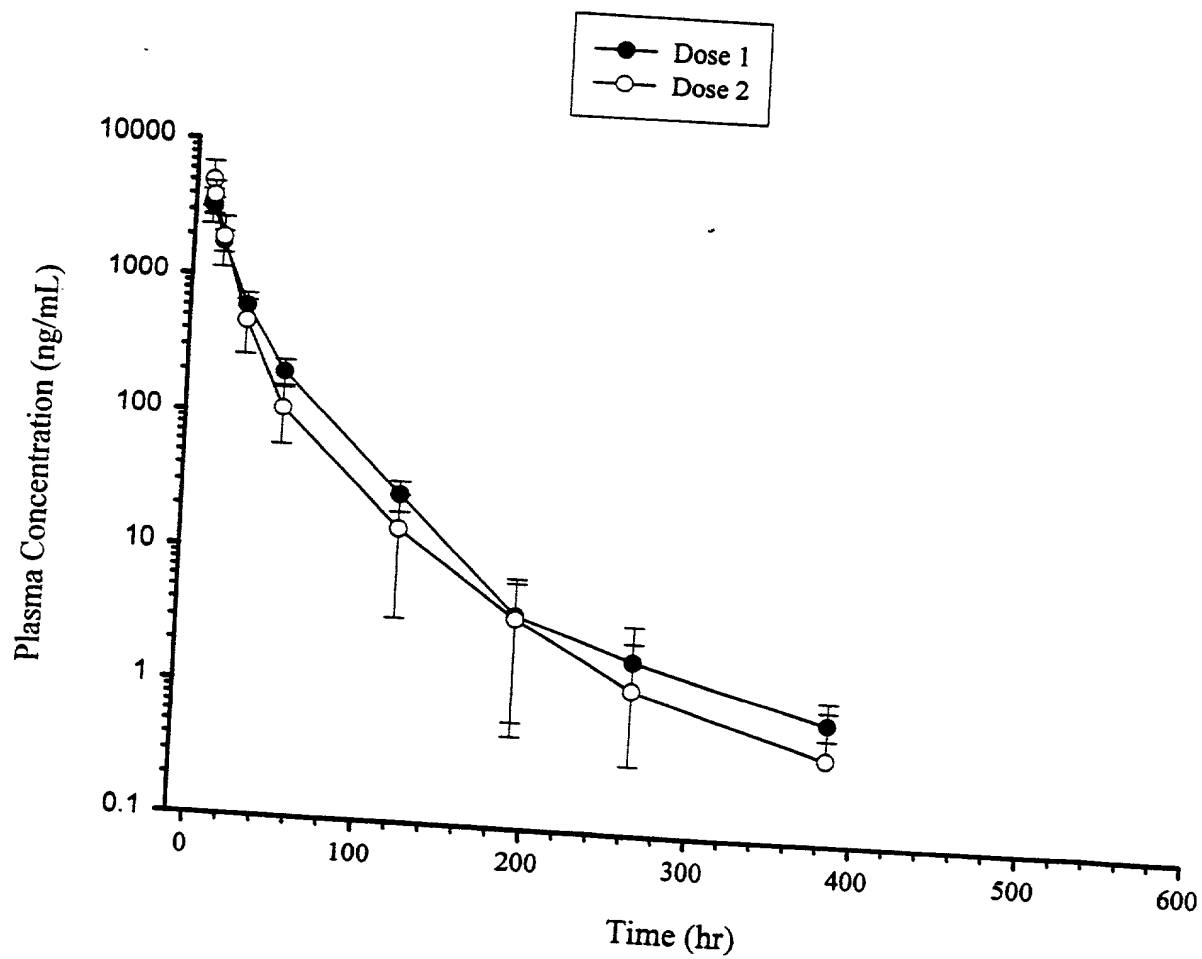


FIG. 13

